

1646

M. Pak

M. Pak

RAW SEQUENCE LISTING DATE: 05/04/2000
 PATENT APPLICATION: US/09/199,874B TIME: 06:18:47

Input Set : A:\Sequence
 Output Set: N:\CRF3\05042000\I199874B.raw

4 <110> APPLICANT: Segre, Gino V.
 5 Kronenberg, Henry M.
 6 Abou-Samra, Abdul-Badi
 7 Juppner, Harald
 8 Potts, Jr., John T.
 9 Schipani, Ernestina
 11 <120> TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
 13 <130> FILE REFERENCE: 00786/071005
 15 <140> CURRENT APPLICATION NUMBER: US 09/199,874B
 16 <141> CURRENT FILING DATE: 1998-11-24
 18 <150> PRIOR APPLICATION NUMBER: US 08/471,494
 19 <151> PRIOR FILING DATE: 1995-06-06
 21 <160> NUMBER OF SEQ ID NOS: 21
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1862
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Didelphoidea
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (98)...(1642)
 34 <400> SEQUENCE: 1
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 36 gtggcccggt tggactcggc ccttagggAAC ggccggcg atg gga gcg ccc cgg atc 115
 37 Met Gly Ala Pro Arg Ile
 38 1 5
 40 tcg cac agc ctt gcc ttg ctc tgc tgc tcc gtg ctc agc tcc gtc 163
 41 Ser His Ser Leu Ala Leu Leu Cys Cys Ser Val Leu Ser Ser Val
 42 10 15 20
 44 tac gca ctg gtg gat gcc gat gat gtc ata acg aag gag gag cag atc 211
 45 Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Glu Gln Ile
 46 25 30 35
 48 att ctt ctg cgc aat gcc cag gac cag tgt gag cag cgc ctg aaa gag 259
 49 Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys Glu Glu Arg Leu Lys Glu
 50 40 45 50
 52 gtc ctc agg gtc cct gaa ctt gct gaa tct gcc aaa gac tgg atg tca 307
 53 Val Leu Arg Val Pro Glu Leu Ala Glu Ser Ala Lys Asp Trp Met Ser
 54 55 60 65 70
 56 agg tct gca aag aca aag aag gag aaa cct gca gaa aag ctt tat ccc 355
 57 Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro Ala Glu Lys Leu Tyr Pro
 58 75 80 85
 60 cag gca gag gag tcc agg gaa gtt tct gac agg agc cgg ctg cag gat 403
 61 Gln Ala Glu Glu Ser Arg Glu Val Ser Asp Arg Ser Arg Leu Gln Asp
 62 90 95 100
 64 ggc ttc tgc cta cct gag tgg gac aac att gtg tgc tgg cct gct gga 451
 65 Gly Phe Cys Leu Pro Glu Trp Asp Asn Ile Val Cys Trp Pro Ala Gly
 66 105 110 115

ENTERED

TC 1000 MAIL ROOM

RECEIVED

MAY 26 2009

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68	gtg	ccc	ggc	aag	gtg	gtg	gcc	gtg	ccc	tgc	ccc	gac	tac	ttc	tac	gac	499	
69	Val	Pro	Gly	Lys	Val	Val	Ala	Val	Pro	Cys	Pro	Asp	Tyr	Phe	Tyr	Asp		
70	120				125							130						
72	tcc	aac	cac	aaa	ggc	cga	gcc	tat	cg	cg	tgt	gac	agc	aat	ggc	agc	547	
73	Phe	Asn	His	Lys	Gly	Arg	Ala	Tyr	Arg	Arg	Cys	Asp	Ser	Asn	Gly	Ser		
74	135					140				145			150					
76	tgg	gag	ctg	gtg	cct	ggg	aac	aac	cg	aca	tgg	g	aat	tac	agc	gaa	595	
77	Trp	Glu	Leu	Val	Pro	Gly	Asn	Asn	Arg	Thr	Trp	Ala	Asn	Tyr	Ser	Glu		
78						155				160			165					
80	tgt	gtc	aag	ttt	ctg	acc	aac	gag	acc	cg	gaa	cg	gaa	gtc	ttt	gat	643	
81	Cys	Val	Lys	Phe	Leu	Thr	Asn	Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp		
82						170				175			180					
84	cgc	ctc	gga	atg	atc	tac	act	gtg	ggc	tac	tcc	atc	tct	ctg	ggc	tcc	691	
85	Arg	Leu	Gly	Met	Ile	Tyr	Thr	Val	Gly	Tyr	Ser	Ile	Ser	Leu	Gly	Ser		
86						185				190			195					
88	ctc	act	gtg	gt	ctg	att	ctg	gg	t	ac	t	ttt	agg	agg	tta	cat	739	
89	Leu	Thr	Val	Ala	Val	Leu	Ile	Leu	Gly	Tyr	Phe	Arg	Arg	Leu	His	Cys		
90						200				205			210					
92	acc	cga	aac	tac	att	cac	atg	cat	ctc	tcc	gtg	tcc	ttt	atg	ctc	cg	787	
93	Thr	Arg	Asn	Tyr	Ile	His	Met	His	Leu	Phe	Val	Ser	Phe	Met	Leu	Arg		
94	215					220				225			230					
96	gct	gt	agc	atc	tcc	atc	aag	gat	gct	gt	ctc	tac	tcg	ggg	gtt	tcc	835	
97	Ala	Val	Ser	Ile	Phe	Ile	Lys	Asp	Ala	Val	Leu	Tyr	Ser	Gly	Val	Ser		
98						235				240			245					
100	aca	gat	gaa	atc	gag	cg	atc	acc	gag	gag	gt	gg	gcc	ttc	aca	883		
101	Thr	Asp	Glu	Ile	Glu	Arg	Ile	Thr	Glu	Glu	Glu	Leu	Arg	Ala	Phe	Thr		
102						250				255			260					
104	gag	cct	ccc	cct	gt	gac	aag	g	cg	gg	t	ttt	gt	gg	tgc	931		
105	Glu	Pro	Pro	Ala	Asp	Iys	Ala	Gly	Phe	Val	Gly	Cys	Arg	Val	Ala			
106						265				270			275					
108	gta	acc	gtc	ttc	ctt	tac	ttc	ctg	acc	acc	aac	tac	tac	tgg	atc	ctg	979	
109	Val	Thr	Val	Phe	Leu	Tyr	Phe	Leu	Thr	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu		
110						280				285			290					
112	gt	gaa	ggc	ctc	tac	ttt	cac	agc	ctc	atc	tcc	atg	gt	ttt	tcc	tct	1027	
113	Val	Glu	Gly	Leu	Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser		
114	295					300				305			310					
116	gag	aaa	aag	tat	ctc	tgg	ggt	tcc	aca	tta	ttt	ggc	tgg	ggc	ctc	cct	1075	
117	Glu	Lys	Lys	Tyr	Leu	Trp	Gly	Phe	Thr	Leu	Phe	Gly	Trp	Gly	Leu	Pro		
118						315				320			325					
120	gcc	gt	ttt	gtc	gt	gt	gt	gt	acc	gt	gg	gt	ac	ctg	ggc	aa	1123	
121	Ala	Val	Phe	Val	Ala	Val	Trp	Val	Thr	Val	Arg	Ala	Thr	Ieu	Ala	Asn		
122						330				335			340					
124	act	gag	tgc	tgg	gac	ctg	agt	tcg	ggg	aat	aag	aaa	tgg	atc	ata	cag	1171	
125	Thr	Glu	Cys	Trp	Asp	Leu	Ser	Ser	Gly	Asn	Lys	Lys	Trp	Ile	Ile	Gln		
126						345				350			355					
128	gt	g	cc	atc	ctg	gca	gct	att	gt	gt	aa	ttt	att	ctt	ttt	atc	aat	1219
129	Val	Pro	Ile	Leu	Ala	Ala	Ile	Val	Val	Asn	Phe	Ile	Leu	Phe	Ile	Asn		
130						360				365			370					
132	ata	atc	aga	gtc	ctg	gct	act	aaa	ctc	cg	gag	acc	aat	gca	ggg	aga	1267	

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133 Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg			
134 375 380 385 390			
136 tgt gac acg agg caa cag tat aga aag ctg ctg aag tcc acg cta gtc			1315
137 Cys Asp Thr Arg Gln Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val			
138 395 400 405			
140 ctc atg ccg cta ttt ggg gtg cac tac atc gtc ttc atg gcc acg ccg			1363
141 Leu Met Pro Leu Phe Gly Val His Tyr Ile Val Phe Met Ala Thr Pro			
142 410 415 420			
144 tac aca gaa gta tca ggg att ctt tgg caa gtc caa atg cac tat gaa			1411
145 Tyr Thr Glu Val Ser Gly Ile Leu Trp Gln Val Gln Met His Tyr Glu			
146 425 430 435			
148 atg ctc ttc aat tca ttc cag gga ttt ttc gtt gcc att ata tac tgt			1459
149 Met Leu Phe Asn Ser Phe Gln Gly Phe Phe Val Ala Ile Tyr Cys			
150 440 445 450			
152 ttc tgc aat gga gag gta caa gca gag atc aag aag tca tgg agc cga			1507
153 Phe Cys Asn Gly Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg			
154 455 460 465 470			
156 tgg acc ctg gcc ttg gac ttc aag cgg aag gcc cgg agt ggc agc agt			1555
157 Trp Thr Leu Ala Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser			
158 475 480 485			
160 acc tac agc tat ggc ccc atg gtg tca cat aca agt gtc acc aat gtg			1603
161 Thr Tyr Ser Tyr Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val			
162 490 495 500			
164 gga cct cga ggg ggc tgg cct tgt ccc tca gcc ctc gac tagctccctgg			1652
165 Gly Pro Arg Gly Gly Trp Pro Cys Pro Ser Ala Leu Asp			
166 505 510 515			
168 ggctggagcc agtggcaatg gccatcacca gttgcctggc tatgtgaagc atgggtccat			1712
169 ttctgagaac tcattgcctt catctggccc agagcctggc accaaagatg acgggtatct			1772
170 caatggctct ggactttatg agccaatgtt tggggaaacag ccccccac tcctggagga			1832
171 ggagagagag acatgtatgtt gaccatatac			1862
173 <210> SEQ ID NO: 2			
174 <211> LENGTH: 1863			
175 <212> TYPE: DNA			
176 <213> ORGANISM: Didelphoidea			
178 <220> FEATURE:			
179 <221> NAME/KEY: CDS			
180 <222> LOCATION: (98)...(1852)			
182 <400> SEQUENCE: 2			
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184 gtggcccggt tggactcggc cctaggaaac ggccggcg atg gga gcg ccc cgg atc		115	
185 Met Gly Ala Pro Arg Ile			
186 1 5			
188 tcg cac agc ctt gcc ttg ctc ctc tgc tgc tcc gtg ctc agc tcc gtc		163	
189 Ser His Ser Leu Ala Leu Leu Leu Cys Cys Ser Val Leu Ser Ser Val			
190 10 15 20			
192 tac gca ctg gtg gat gcc gat gat gtc ata acg aag gag gag cag atc		211	
193 Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Glu Gln Ile			
194 25 30 35			
196 att ctt ctg cgc aat gcc cag gcc cag tgt gag cag cgc ctg aaa gag		259	

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197 Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys Glu Gln Arg Leu Lys Glu		
198 40 45 50		
200 gtc ctc agg gtc cct gaa ctt gct gaa tct gcc aaa gac tgg atg tca	307	
201 Val Leu Arg Val Pro Glu Leu Ala Glu Ser Ala Lys Asp Trp Met Ser		
202 55 60 65 70		
204 agg tct gca aag aca aag aag gag aaa cct gca gaa aag ctt tat ccc	355	
205 Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro Ala Glu Lys Leu Tyr Pro		
206 75 80 85		
208 cag gca gag gag tcc agg gaa gtt tct gac agg agc cgg ctg cag gat	403	
209 Gln Ala Glu Glu Ser Arg Glu Val Ser Asp Arg Ser Arg Leu Gln Asp		
210 90 95 100		
212 ggc ttc tgc cta cct gag tgg gac aac att gtg tgc tgg cct gct gga	451	
213 Gly Phe Cys Leu Pro Glu Trp Asp Asn Ile Val Cys Trp Pro Ala Gly		
214 105 110 115		
216 gtg ccc ggc aag gtg gtg gcc gtg ccc tgc ccc gac tac ttc tac gac	499	
217 Val Pro Gly Lys Val Val Ala Val Pro Cys Pro Asp Tyr Phe Tyr Asp		
218 120 125 130		
220 ttc aac cac aaa ggc cga gcc tat cgg cgc tgt gac agc aat ggc agc	547	
221 Phe Asn His Lys Gly Arg Ala Tyr Arg Arg Cys Asp Ser Asn Gly Ser		
222 135 140 145 150		
224 tgg gag ctg gtg cct ggg aac aac cgg aca tgg gcg aat tac agc gaa	595	
225 Trp Glu Leu Val Pro Gly Asn Asn Arg Thr Trp Ala Asn Tyr Ser Glu		
226 155 160 165		
228 tgt gtc aag ttt ctg acc aac gag acc cgg gaa cgg gaa gtc ttt gat	643	
229 Cys Val Lys Phe Leu Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp		
230 170 175 180		
232 cgc ctc gga atg atc tac act gtg ggc tac tcc atc tct ctg ggc tcc	691	
233 Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Ile Ser Leu Gly Ser		
234 185 190 195		
236 ctc act gtg gct gtg ctg att ctg ggt tac ttt agg agg tta cat tgc	739	
237 Leu Thr Val Ala Val Ile Leu Gly Tyr Phe Arg Arg Leu His Cys		
238 200 205 210		
240 acc cga aac tac att cac atg cat ctc ttc gtg tcc ttt atg ctc cgg	787	
241 Thr Arg Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg		
242 215 220 225 230		
244 gct gta agc atc ttc atc aag gat gct gtg ctc tac tcg ggg gtt tcc	835	
245 Ala Val Ser Ile Phe Ile Lys Asp Ala Val Leu Tyr Ser Gly Val Ser		
246 235 240 245		
248 aca gat gaa atc gag cgc atc acc gag gag gag ctg agg gcc ttc aca	883	
249 Thr Asp Glu Ile Glu Arg Ile Thr Glu Glu Leu Arg Ala Phe Thr		
250 250 255 260		
252 gag cct ccc cct gct gac aag gcg ggt ttt gtg ggc tgc aga gtg gcg	931	
253 Glu Pro Pro Ala Asp Lys Ala Gly Phe Val Gly Cys Arg Val Ala		
254 265 270 275		
256 gta acc gtc ttc ctt tac ttc ctg acc acc aac tac tac tgg atc ctg	979	
257 Val Thr Val Phe Leu Tyr Phe Leu Thr Thr Asn Tyr Tyr Trp Ile Leu		
258 280 285 290		
260 gtg gaa ggc ctc tac ctt cac agc ctc atc ttc atg gct ttt ttc tct	1027	
261 Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser		

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262	295	300	305	310													
264	gag	aaa	aag	tat	ctc	tgg	ggt	ttc	aca	tta	ttt	ggc	ttg	ggc	ctc	cct	1075
265	Glu	Lys	Lys	Tyr	Leu	Trp	Gly	Phe	Thr	Leu	Phe	Gly	Trp	Gly	Leu	Pro	
266																	315
268	gcc	gtg	ttt	gtc	gct	gtg	ttg	gtg	acc	gtg	agg	gtc	aca	ctg	gcc	aac	1123
269	Ala	Val	Phe	Val	Ala	Val	Trp	Val	Thr	Val	Arg	Ala	Thr	Leu	Ala	Asn	
270																330	
272	act	gag	tgc	tgg	gac	ctg	agt	tcg	ggg	aat	aag	aaa	tgg	atc	ata	cag	1171
273	Thr	Glu	Cys	Trp	Asp	Leu	Ser	Ser	Gly	Asn	Lys	Lys	Trp	Ile	Ile	Gln	
274																345	
276	gtg	ccc	atc	ctg	gca	gct	act	aaa	ctc	cg	gag	acc	aat	gca	ggg	aga	1219
277	Val	Pro	Ile	Leu	Ala	Ala	Ile	Val	Val	Asn	Phe	Ile	Leu	Phe	Ile	Asn	
278																360	
280	ata	atc	aga	gtc	ctg	gct	act	aaa	ctc	cg	gag	acc	aat	gca	ggg	aga	1267
281	Ile	Ile	Arg	Val	Leu	Ala	Thr	Lys	Leu	Arg	Glu	Thr	Asn	Ala	Gly	Arg	
282																375	
284	tgt	gac	acg	agg	caa	cag	tat	aga	aag	ctg	ctg	aag	tcc	acg	cta	gtc	1315
285	Cys	Asp	Thr	Arg	Gln	Gln	Tyr	Arg	Lys	Leu	Leu	Lys	Ser	Thr	Leu	Val	
286																395	
288	ctc	atg	ccg	cta	ttt	ggg	gtg	cac	tac	atc	gtc	ttc	atg	gcc	acg	ccg	1363
289	Leu	Met	Pro	Leu	Phe	Gly	Val	His	Tyr	Ile	Val	Phe	Met	Ala	Thr	Pro	
290																410	
292	tac	aca	gaa	gt	ta	ca	gg	ttt	ttc	gtt	gcc	att	ata	tac	tgt		1411
293	Tyr	Thr	Glu	Val	Ser	Gly	Ile	Leu	Trp	Gln	Val	Gln	Met	His	Tyr	Glu	
294																425	
296	atg	ctc	tcc	aat	tca	tcc	cag	gga	ttt	ttc	gtt	gcc	att	ata	tac	tgt	1459
297	Met	Leu	Phe	Asn	Ser	Phe	Gln	Gly	Phe	Phe	Val	Ala	Ile	Ile	Tyr	Cys	
298																440	
300	ttc	tgc	aat	gga	gag	gt	ta	ca	ttt	ttc	gtt	gcc	att	ata	tac	tgt	1507
301	Phe	Cys	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Lys	Ser	Trp	Ser	Arg	
302																455	
304	tgg	acc	ctg	gcc	ttt	gac	tcc	aag	cg	aag	gcc	cg	agt	ggc	acg	agt	1555
305	Trp	Thr	Leu	Ala	Leu	Asp	Phe	Lys	Arg	Lys	Ala	Arg	Ser	Gly	Ser	Ser	
306																475	
308	acc	tac	agc	tat	ggc	ccc	atg	gtg	tca	cat	aca	agt	gtc	acc	aat	gtg	1603
309	Thr	Tyr	Ser	Tyr	Gly	Pro	Met	Val	Ser	His	Thr	Ser	Val	Thr	Asn	Val	
310																490	
312	gga	cct	cga	ggg	ggg	ctg	gcc	ttt	tcc	ctc	agc	cct	cga	cta	gt	cct	1651
313	Gly	Pro	Arg	Gly	Gly	Leu	Ala	Leu	Ser	Leu	Ser	Pro	Arg	Leu	Ala	Pro	
314																505	
316	ggg	gct	gga	gcc	agt	ggc	aat	ggc	cat	cac	cag	ttt	cct	ggc	tat	gtg	1699
317	Gly	Ala	Gly	Ala	Ser	Ala	Asn	Gly	His	His	Gln	Leu	Pro	Gly	Tyr	Val	
318																520	
320	aag	cat	ggt	tcc	att	tct	gag	aac	tca	ttt	cct	tca	tct	ggc	cca	gag	1747
321	Lys	His	Gly	Ser	Ile	Ser	Glu	Asn	Ser	Leu	Pro	Ser	Ser	Gly	Pro	Glu	
322																535	
324	cct	ggc	acc	aaa	gat	gac	ggg	tat	ctc	aat	ggc	tct	gga	ctt	tat	gag	1795
325	Pro	Gly	Thr	Lys	Asp	Asp	Gly	Tyr	Leu	Asn	Gly	Ser	Gly	Leu	Tyr	Glu	
326																555	

✓

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/199,874B DATE: 05/04/2000
TIME: 06:18:48

Input Set : A:\Sequence
Output Set: N:\CRF3\05042000\I199874B.raw

L:724 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8